

SEQUENCE LISTING

<110> MASAI, Hisao

TAMAI Katsuyuki

<120> Cdc7-ASK KINASE COMPLEX, SUBSTRATES OF THE KINASE COMPLEX,  
SPECIFIC ANTIBODIES TO THE SUBSTRATES, AND SCREENING METHODS  
USING THE SAME TO SCREEN FOR COMPOUNDS COMPRISING Cdc7-ASK  
KINASE INHIBITORY ABILITY

<130> M3-A0201P

<140>

<141>

<150> JP 2002-067702

<151> 2002-03-12

<160> 21

<170> PatentIn Ver. 2.1

<210> 1

<211> 130

<212> PRT

<213> Homo sapiens

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Ser Ser Pro Gly Arg Ser Ser Arg Arg Thr Asp Ala Leu Thr Ser Ser

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Pro Gly Arg Asp Leu Pro Pro Phe Glu Asp Glu Ser Glu Gly Leu Leu

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Gly Thr Glu Gly Pro Leu Glu Glu Glu Glu Asp Gly Glu Glu Leu Ile

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Gly Asp Gly Met Glu Arg Asp Tyr Arg Ala Ile Pro Glu Leu Asp Ala

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Tyr Glu Ala Glu Gly Leu Ala Leu Asp Asp Glu Asp Val Glu Glu Leu

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95

Thr Ala Ser Gln Arg Glu Ala Ala Glu Arg Ala Met Arg Gln Arg Asp

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Arg Glu Ala Gly Arg Gly Leu Gly Arg Met Arg Arg Gly Leu Leu Tyr

115

120

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Asp Ser

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&lt;210&gt; 2

&lt;211&gt; 3379

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (31).. (2709)

&lt;400&gt; 2

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Met Ala Ser Ser Pro Ala Gln Arg

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Arg Arg Gly Asn Asp Pro Leu Thr Ser Ser Pro Gly Arg Ser Ser Arg

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cgt act gat gcc ctc acc tcc agc cct ggc cgt gac ctt cca cca ttt 150

Arg Thr Asp Ala Leu Thr Ser Ser Pro Gly Arg Asp Leu Pro Pro Phe

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gag gat gag tcc gag ggg ctc cta ggc aca gag ggg ccc ctg gag gaa 198

Glu Asp Glu Ser Glu Gly Leu Leu Gly Thr Glu Gly Pro Leu Glu Glu

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gaa gag gat gga gag gag ctc att gga gat ggc atg gaa agg gac tac 246

Glu Glu Asp Gly Glu Glu Leu Ile Gly Asp Gly Met Glu Arg Asp Tyr

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65

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cgc gcc atc cca gag ctg gac gcc tat gag gcc gag gga ctg gct ctg 294

Arg Ala Ile Pro Glu Leu Asp Ala Tyr Glu Ala Glu Gly Leu Ala Leu

75

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85

gat gat gag gac gta gag gag ctg acg gcc agt cga agg gag gca gca 342

Asp Asp Glu Asp Val Glu Glu Leu Thr Ala Ser Arg Arg Glu Ala Ala

90

95

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gac ggg cca tgc ggc acg gtg acc ggg agc tgg ccg ggg ctg ggc gca 390

Asp Gly Pro Cys Gly Thr Val Thr Gly Ser Trp Pro Gly Leu Gly Ala

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tgc gcc gtg ggc tcc tgt atg aca gcg atg agg agg acg agg agc gcc 438

Cys Ala Val Gly Ser Cys Met Thr Ala Met Arg Arg Thr Arg Ser Ala

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ctg ccc gca agc gcc gcc agt gga gcc ggc acg gag gac ggc gag gag 486

Leu Pro Ala Ser Ala Ala Ser Gly Ala Gly Thr Glu Asp Gly Glu Glu

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gac gag cag atg att gag agc atc gag aac ctg gag gat ctc aaa ggc			534
Asp Glu Gln Met Ile Glu Ser Ile Glu Asn Leu Glu Asp Leu Lys Gly			
155	160	165	
cac tct gtg cgc gag tgg gtg agc atg gcg ggc ccc cgg ctg gag atc			582
His Ser Val Arg Glu Trp Val Ser Met Ala Gly Pro Arg Leu Glu Ile			
170	175	180	
cac cac cgc ttc aag aac ttc ctg cgc act cac gtc gac agc cac ggc			630
His His Arg Phe Lys Asn Phe Leu Arg Thr His Val Asp Ser His Gly			
185	190	195	200
cac aac gtc ttc aag gag cgc atc agc gac atg tgc aaa gag aac cgt			678
His Asn Val Phe Lys Glu Arg Ile Ser Asp Met Cys Lys Glu Asn Arg			
205	210	215	
gag agc ctg gtg gtg aac tat gag gac ttg gca gcc agg gag cac gtg			726
Glu Ser Leu Val Val Asn Tyr Glu Asp Leu Ala Ala Arg Glu His Val			
220	225	230	
ctg gcc tac ttc ctg cct gag gca ccg gcg gag ctg ctg cag atc ttt			774
Leu Ala Tyr Phe Leu Pro Glu Ala Pro Ala Glu Leu Leu Gln Ile Phe			
235	240	245	

gat gag gct gcc ctg gag gtg gta ctg gcc atg tac ccc aag tac gac 822

Asp Glu Ala Ala Leu Glu Val Val Leu Ala Met Tyr Pro Lys Tyr Asp

250

255

260

cgc atc acc aac cac atc cat gtc cgc atc tcc cac ctg cct ctg gtg 870

Arg Ile Thr Asn His Ile His Val Arg Ile Ser His Leu Pro Leu Val

265

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275

280

gag gag ctg cgc tcg ctg agg cag ctg cat ctg aac cag ctg atc cgc 918

Glu Glu Leu Arg Ser Leu Arg Gln Leu His Leu Asn Gln Leu Ile Arg

285

290

295

acc agt ggg gtg gtg acc agc tgc act ggc gtc ctg ccc cag ctc agc 966

Thr Ser Gly Val Val Thr Ser Cys Thr Gly Val Leu Pro Gln Leu Ser

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305

310

atg gtc aag tac aac tgc aac aag tgc aat ttc gtc ctg ggt cct ttc 1014

Met Val Lys Tyr Asn Cys Asn Lys Cys Asn Phe Val Leu Gly Pro Phe

315

320

325

tgc cag tcc cag aac cag gag gtg aaa cca ggc tcc tgt cct gag tgc 1062

Cys Gln Ser Gln Asn Gln Glu Val Lys Pro Gly Ser Cys Pro Glu Cys

330

335

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cag tcg gcc ggc ccc ttt gag gtc aac atg gag gag acc atc tat cag 1110

Gln Ser Ala Gly Pro Phe Glu Val Asn Met Glu Glu Thr Ile Tyr Gln

345	350	355	360	
aac tac cag cgt atc cga atc cag gag agt cca ggc aaa gtg gcg gct				1158
Asn Tyr Gln Arg Ile Arg Ile Gln Glu Ser Pro Gly Lys Val Ala Ala				
	365	370	375	
cgg cgg ctg ccc cgc tcc aag gac gcc att ctc ctc gca gat ctg gtg				1206
Arg Arg Leu Pro Arg Ser Lys Asp Ala Ile Leu Leu Ala Asp Leu Val				
	380	385	390	
gac agc tgc aac gca gga gac gag ata gag ctg act ggc atc tat cac				1254
Asp Ser Cys Asn Ala Gly Asp Glu Ile Glu Leu Thr Gly Ile Tyr His				
	395	400	405	
aac aac tat gat ggc tcc ctc aac act gcc aat ggc ttc cct gtc ttt				1302
Asn Asn Tyr Asp Gly Ser Leu Asn Thr Ala Asn Gly Phe Pro Val Phe				
	410	415	420	
gcc act gtc atc cta gcc aac cac gtg gcc aag aag gac aac aag gtt				1350
Ala Thr Val Ile Leu Ala Asn His Val Ala Lys Lys Asp Asn Lys Val				
	425	430	435	440
gct gta ggg gaa ctg acc gat gaa gat gtg aag atg atc act agc ctc				1398
Ala Val Gly Glu Leu Thr Asp Glu Asp Val Lys Met Ile Thr Ser Leu				
	445	450	455	

tcc aag gat cag cag atc gga gag aag atc ttt gcc agc att gct cct 1446

Ser Lys Asp Gln Gln Ile Gly Glu Lys Ile Phe Ala Ser Ile Ala Pro

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tcc atc tat ggt cat gaa gac atc aag aga ggc cct gct ctg gcc ctg 1494

Ser Ile Tyr Gly His Glu Asp Ile Lys Arg Gly Pro Ala Leu Ala Leu

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ttc gga ggg gag ccc aaa aac cca ggt ggc aag cac aag gta cgt ggt 1542

Phe Gly Gly Glu Pro Lys Asn Pro Gly Gly Lys His Lys Val Arg Gly

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gat atc aac gtg ctc ttg tgc gga gac cct ggc aca gcg aag tcg cag 1590

Asp Ile Asn Val Leu Leu Cys Gly Asp Pro Gly Thr Ala Lys Ser Gln

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ttt ctc aag tat att gag aaa gtg tcc agc cga gcc atc ttc acc act 1638

Phe Leu Lys Tyr Ile Glu Lys Val Ser Ser Arg Ala Ile Phe Thr Thr

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ggc cag ggg gcg tcg gct gtg gcc gtc acg gcg tat gtc cag cgg cac 1686

Gly Gln Gly Ala Ser Ala Val Ala Val Thr Ala Tyr Val Gln Arg His

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cct gtc agc agg gag tgg acc ttg gag gct ggg gcc ctg gtt ctg gct 1734

Pro Val Ser Arg Glu Trp Thr Leu Glu Ala Gly Ala Leu Val Leu Ala

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gac cga gga gtg tgt ctc att gat gaa ttt gac aag atg aat gac cag 1782

Asp Arg Gly Val Cys Leu Ile Asp Glu Phe Asp Lys Met Asn Asp Gln

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gac aga acc agc atc cat gag gcc atg gag caa cag agc atc tcc atc 1830

Asp Arg Thr Ser Ile His Glu Ala Met Glu Gln Gln Ser Ile Ser Ile

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tcg aag gct ggc atc gtc acc tcc ctg cag gct cgc tgc acg gtc att 1878

Ser Lys Ala Gly Ile Val Thr Ser Leu Gln Ala Arg Cys Thr Val Ile

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gct gcc gcc aac ccc ata gga ggg cgc tac gac ccc tcg ctg act ttc 1926

Ala Ala Ala Asn Pro Ile Gly Gly Arg Tyr Asp Pro Ser Leu Thr Phe

620

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tct gag aac gtg gac ctc aca gag ccc atc atc tca cgc ttt gac atc 1974

Ser Glu Asn Val Asp Leu Thr Glu Pro Ile Ile Ser Arg Phe Asp Ile

635

640

645

ctg tgt gtg gtg agg gac acc gtg gac cca gtc cag gac gag atg ctg 2022

Leu Cys Val Val Arg Asp Thr Val Asp Pro Val Gln Asp Glu Met Leu

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gcc cgc ttc gtg gtg ggc agc cac gtc aga cac cac ccc agc aac aag 2070

Ala Arg Phe Val Val Gly Ser His Val Arg His His Pro Ser Asn Lys

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670

675

680

gag gag gag ggg ctg gcc aat ggc agc gct gct gag ccc gcc atg ccc 2118

Glu Glu Glu Gly Leu Ala Asn Gly Ser Ala Ala Glu Pro Ala Met Pro

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aac acg tat ggc gtg gag ccc ctg ccc cag gag gtc ctg aag aag tac 2166

Asn Thr Tyr Gly Val Glu Pro Leu Pro Gln Glu Val Leu Lys Lys Tyr

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atc atc tac gcc aag gag agg gtc cac ccg aag ctc aac cag atg gac 2214

Ile Ile Tyr Ala Lys Glu Arg Val His Pro Lys Leu Asn Gln Met Asp

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cag gac aag gtg gcc aag atg tac agt gac ctg agg aaa gaa tct atg 2262

Gln Asp Lys Val Ala Lys Met Tyr Ser Asp Leu Arg Lys Glu Ser Met

730

735

740

gcg aca ggc agc atc ccc att acg gtg cgg cac atc gag tcc atg agt 2310

Ala Thr Gly Ser Ile Pro Ile Thr Val Arg His Ile Glu Ser Met Ser

745

750

755

760

cat ggc gga ggc cca cgc gcg cat cca tct gcg gga cta tgt gat cga 2358

His Gly Gly Gly Pro Arg Ala His Pro Ser Ala Gly Leu Cys Asp Arg

765	770	775	
aga cga cgt caa cat ggc cat ccg cgt gat gct gga gag ctt cat aga			2406
Arg Arg Arg Gln His Gly His Pro Arg Asp Ala Gly Glu Leu His Arg			
780	785	790	
cac aca gaa gtt cag cgt cat cgc agc atg cgc aag act ttt gcc cgc			2454
His Thr Glu Val Gln Arg His Arg Ser Met Arg Lys Thr Phe Ala Arg			
795	800	805	
tac ctt tca ttc cgg cgt gac aac aat gag ctg ttg ctc ttc ata ctg			2502
Tyr Leu Ser Phe Arg Arg Asp Asn Asn Glu Leu Leu Leu Phe Ile Leu			
810	815	820	
aag cag tta gtg gca gag cag gtg aca tat cag cgc aac cgc ttt ggg			2550
Lys Gln Leu Val Ala Glu Gln Val Thr Tyr Gln Arg Asn Arg Phe Gly			
825	830	835	840
gcc cag cag gac act att gag gtc cct gag aag gac ttg gtg gat aag			2598
Ala Gln Gln Asp Thr Ile Glu Val Pro Glu Lys Asp Leu Val Asp Lys			
845	850	855	
gct cgt cag atc aac atc cac aac ctc tct gca ttt tat gac agt gag			2646
Ala Arg Gln Ile Asn Ile His Asn Leu Ser Ala Phe Tyr Asp Ser Glu			
860	865	870	

ctc ttc agg atg aac aag ttc agc cac gac ctg aaa agg aaa atg atc 2694

Leu Phe Arg Met Asn Lys Phe Ser His Asp Leu Lys Arg Lys Met Ile

875

880

885

ctg cag cag ttc tga ggcctatgc catccataag gattccttgg gattctggtt 2749

Leu Gln Gln Phe

890

tggggtggtc agtgccctct gtgctttatg gacacaaaac cagagcactt gatgaactcg 2809

gggtactagg gtcagggtt atagcaggat gtctggctgc acctggcatg actgtttgtt 2869

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<210> 3

<211> 892

<212> PRT

<213> Homo sapiens

&lt;400&gt; 3

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Ser Ser Pro Gly Arg Ser Ser Arg Arg Thr Asp Ala Leu Thr Ser Ser

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Pro Gly Arg Asp Leu Pro Pro Phe Glu Asp Glu Ser Glu Gly Leu Leu

35 40 45

Gly Thr Glu Gly Pro Leu Glu Glu Glu Glu Asp Gly Glu Glu Leu Ile

50 55 60

Gly Asp Gly Met Glu Arg Asp Tyr Arg Ala Ile Pro Glu Leu Asp Ala

65 70 75 80

Tyr Glu Ala Glu Gly Leu Ala Leu Asp Asp Glu Asp Val Glu Glu Leu

85 90 95

Thr Ala Ser Arg Arg Glu Ala Ala Asp Gly Pro Cys Gly Thr Val Thr

100 105 110

Gly Ser Trp Pro Gly Leu Gly Ala Cys Ala Val Gly Ser Cys Met Thr

115 120 125

Ala Met Arg Arg Thr Arg Ser Ala Leu Pro Ala Ser Ala Ala Ser Gly

130 135 140

Ala Gly Thr Glu Asp Gly Glu Glu Asp Glu Gln Met Ile Glu Ser Ile

145 150 155 160

Glu Asn Leu Glu Asp Leu Lys Gly His Ser Val Arg Glu Trp Val Ser

165 170 175

Met Ala Gly Pro Arg Leu Glu Ile His His Arg Phe Lys Asn Phe Leu

180 185 190

Arg Thr His Val Asp Ser His Gly His Asn Val Phe Lys Glu Arg Ile

195	200	205
Ser Asp Met Cys Lys Glu Asn Arg Glu Ser Leu Val Val Asn Tyr Glu		
210	215	220
Asp Leu Ala Ala Arg Glu His Val Leu Ala Tyr Phe Leu Pro Glu Ala		
225	230	235
Pro Ala Glu Leu Leu Gln Ile Phe Asp Glu Ala Ala Leu Glu Val Val		
245	250	255
Leu Ala Met Tyr Pro Lys Tyr Asp Arg Ile Thr Asn His Ile His Val		
260	265	270
Arg Ile Ser His Leu Pro Leu Val Glu Glu Leu Arg Ser Leu Arg Gln		
275	280	285
Leu His Leu Asn Gln Leu Ile Arg Thr Ser Gly Val Val Thr Ser Cys		
290	295	300
Thr Gly Val Leu Pro Gln Leu Ser Met Val Lys Tyr Asn Cys Asn Lys		
305	310	315
Cys Asn Phe Val Leu Gly Pro Phe Cys Gln Ser Gln Asn Gln Glu Val		
325	330	335
Lys Pro Gly Ser Cys Pro Glu Cys Gln Ser Ala Gly Pro Phe Glu Val		
340	345	350
Asn Met Glu Glu Thr Ile Tyr Gln Asn Tyr Gln Arg Ile Arg Ile Gln		
355	360	365
Glu Ser Pro Gly Lys Val Ala Ala Arg Arg Leu Pro Arg Ser Lys Asp		
370	375	380
Ala Ile Leu Leu Ala Asp Leu Val Asp Ser Cys Asn Ala Gly Asp Glu		
385	390	395
Ile Glu Leu Thr Gly Ile Tyr His Asn Asn Tyr Asp Gly Ser Leu Asn		

405	410	415
Thr Ala Asn Gly Phe Pro Val Phe Ala Thr Val Ile Leu Ala Asn His		
420	425	430
Val Ala Lys Lys Asp Asn Lys Val Ala Val Gly Glu Leu Thr Asp Glu		
435	440	445
Asp Val Lys Met Ile Thr Ser Leu Ser Lys Asp Gln Gln Ile Gly Glu		
450	455	460
Lys Ile Phe Ala Ser Ile Ala Pro Ser Ile Tyr Gly His Glu Asp Ile		
465	470	475
Lys Arg Gly Pro Ala Leu Ala Leu Phe Gly Gly Glu Pro Lys Asn Pro		
485	490	495
Gly Gly Lys His Lys Val Arg Gly Asp Ile Asn Val Leu Leu Cys Gly		
500	505	510
Asp Pro Gly Thr Ala Lys Ser Gln Phe Leu Lys Tyr Ile Glu Lys Val		
515	520	525
Ser Ser Arg Ala Ile Phe Thr Thr Gly Gln Gly Ala Ser Ala Val Ala		
530	535	540
Val Thr Ala Tyr Val Gln Arg His Pro Val Ser Arg Glu Trp Thr Leu		
545	550	555
Glu Ala Gly Ala Leu Val Leu Ala Asp Arg Gly Val Cys Leu Ile Asp		
565	570	575
Glu Phe Asp Lys Met Asn Asp Gln Asp Arg Thr Ser Ile His Glu Ala		
580	585	590
Met Glu Gln Gln Ser Ile Ser Ile Ser Lys Ala Gly Ile Val Thr Ser		
595	600	605
Leu Gln Ala Arg Cys Thr Val Ile Ala Ala Ala Asn Pro Ile Gly Gly		

610	615	620	
Arg Tyr Asp Pro Ser	Leu Thr Phe Ser Glu Asn Val	Asp Leu Thr Glu	
625	630	635	640
Pro Ile Ile Ser Arg Phe	Asp Ile Leu Cys Val Val Arg	Asp Thr Val	
	645	650	655
Asp Pro Val Gln Asp	Glu Met Leu Ala Arg Phe Val Val	Gly Ser His	
	660	665	670
Val Arg His His Pro Ser	Asn Lys Glu Glu Glu Gly Leu Ala Asn	Gly	
	675	680	685
Ser Ala Ala Glu Pro Ala	Met Pro Asn Thr Tyr Gly Val Glu Pro	Leu	
	690	695	700
Pro Gln Glu Val Leu Lys	Lys Tyr Ile Ile Tyr Ala Lys Glu Arg	Val	
705	710	715	720
His Pro Lys Leu Asn Gln	Met Asp Gln Asp Lys Val Ala Lys Met	Tyr	
	725	730	735
Ser Asp Leu Arg Lys Glu	Ser Met Ala Thr Gly Ser Ile Pro Ile Thr		
	740	745	750
Val Arg His Ile Glu Ser	Met Ser His Gly Gly Gly Pro Arg Ala His		
	755	760	765
Pro Ser Ala Gly Leu Cys	Asp Arg Arg Arg Gln His Gly His Pro		
	770	775	780
Arg Asp Ala Gly Glu Leu	His Arg His Thr Glu Val Gln Arg His Arg		
785	790	795	800
Ser Met Arg Lys Thr Phe	Ala Arg Tyr Leu Ser Phe Arg Arg Asp Asn		
	805	810	815
Asn Glu Leu Leu Leu Phe	Ile Leu Lys Gln Leu Val Ala Glu Gln Val		

17 / 59

820	825	830	
Thr Tyr Gln Arg Asn Arg Phe Gly Ala Gln Gln Asp Thr Ile Glu Val			
835	840	845	
Pro Glu Lys Asp Leu Val Asp Lys Ala Arg Gln Ile Asn Ile His Asn			
850	855	860	
Leu Ser Ala Phe Tyr Asp Ser Glu Leu Phe Arg Met Asn Lys Phe Ser			
865	870	875	880
His Asp Leu Lys Arg Lys Met Ile Leu Gln Gln Phe			
885	890		

<210> 4

<211> 2715

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(2715)

<400> 4

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Met Ala Glu Ser Ser Glu Ser Leu Ser Ala Ser Ser Pro Ala Arg Gln

1 5 10 15

cgg cgc cgg atc agt gat ccc ctc acc tcc agc cca ggc cgc agc tcc 96

1 8 / 5 9

Arg Arg Arg Ile Ser Asp Pro Leu Thr Ser Ser Pro Gly Arg Ser Ser

20

25

30

aga cgt gct gac gcc ctg acc tcc agc cct ggc aga gac ctc ccc cca 144

Arg Arg Ala Asp Ala Leu Thr Ser Ser Pro Gly Arg Asp Leu Pro Pro

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ttt gaa gat gag tct gag ggg ctt ctg ggc aca gag ggg ccc atg gag 192

Phe Glu Asp Glu Ser Glu Gly Leu Leu Gly Thr Glu Gly Pro Met Glu

50

55

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gaa gaa gag gat gga gag gaa ctc att ggt gat ggc atg gag aga gac 240

Glu Glu Glu Asp Gly Glu Glu Leu Ile Gly Asp Gly Met Glu Arg Asp

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70

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tac cgt ccc att ccg gag ctc gat gtc tac gag gcc gag gga ttg gcc 288

Tyr Arg Pro Ile Pro Glu Leu Asp Val Tyr Glu Ala Glu Gly Leu Ala

85

90

95

ctg gat gat gaa gat gtg gag gag ctg aca gcc agt cag aga gag gca 336

Leu Asp Asp Glu Asp Val Glu Glu Leu Thr Ala Ser Gln Arg Glu Ala

100

105

110

gct gag cgg acc atg agg cag cgg gac cgt gag gct ggc aga ggc ctg 384

Ala Glu Arg Thr Met Arg Gln Arg Asp Arg Glu Ala Gly Arg Gly Leu

115

120

125

gga cgc atg cgc cgg. ggg ctg ctc tat gac agc agc gag gaa gat gag 432

Gly Arg Met Arg Arg Gly Leu Leu Tyr Asp Ser Ser Glu Glu Asp Glu

130

135

140

gag cgg cct gcc cgt aag cgc cgc cac gta gaa cgc gcc aca gag gat 480

Glu Arg Pro Ala Arg Lys Arg Arg His Val Glu Arg Ala Thr Glu Asp

145

150

155

160

ggc gag gag gat gaa gag atg atc gag agt att gag aat ctg gag gac 528

Gly Glu Glu Asp Glu Glu Met Ile Glu Ser Ile Glu Asn Leu Glu Asp

165

170

175

ctc aag ggc cac tcg gtg cgc gag cgg gtg agc atg gca ggg ccc agg 576

Leu Lys Gly His Ser Val Arg Glu Arg Val Ser Met Ala Gly Pro Arg

180

185

190

ctg gag atc cac cac cgc ttc aag aac ttc ctg cgc acc cac gtg gac 624

Leu Glu Ile His His Arg Phe Lys Asn Phe Leu Arg Thr His Val Asp

195

200

205

agc cat ggc cac aac gtc ttc aag gag cgc atc agt gat atg tgc aaa 672

Ser His Gly His Asn Val Phe Lys Glu Arg Ile Ser Asp Met Cys Lys

210

215

220

gag aac cgt gag agt ttg gtg gta aat tat gaa gac ctg gca gcc cgg 720

Glu Asn Arg Glu Ser Leu Val Val Asn Tyr Glu Asp Leu Ala Ala Arg

225 230 235 240

gag cac gtg ttg gca tac ttc ctg ccg gaa gca ccg gct gag ttg ctg 768

Glu His Val Leu Ala Tyr Phe Leu Pro Glu Ala Pro Ala Glu Leu Leu

245 250 255

cag atc ttt gac gag gct gcc ctg gag gtc gtg ttg gcc atg tac cct 816

Gln Ile Phe Asp Glu Ala Ala Leu Glu Val Val Leu Ala Met Tyr Pro

260 265 270

aaa tat gac cgt atc acc aac cac atc cat gtg cgc atc tcc cac ctg 864

Lys Tyr Asp Arg Ile Thr Asn His Ile His Val Arg Ile Ser His Leu

275 280 285

cct ctg gtg gag gag ctg cgt tca ctg agg cag ttg cac ctg aac cag 912

Pro Leu Val Glu Glu Leu Arg Ser Leu Arg Gln Leu His Leu Asn Gln

290 295 300

ctg atc cgt acc agt ggc gtg gtg acc agc tgc acc gga gtc ctg ccc 960

Leu Ile Arg Thr Ser Gly Val Val Thr Ser Cys Thr Gly Val Leu Pro

305 310 315 320

cag ctc agc atg gtc aag tac aac tgt agc aag tgc aac ttt gta ctg 1008

Gln Leu Ser Met Val Lys Tyr Asn Cys Ser Lys Cys Asn Phe Val Leu

325 330 335

ggg cct ttc tgc cag tct cag aat cag gag gtg aag cct ggc tcc tgc 1056

Gly Pro Phe Cys Gln Ser Gln Asn Gln Glu Val Lys Pro Gly Ser Cys

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cct gag tgc cag tct gct ggg ccc ttt gag atc aac atg gag gag acc 1104

Pro Glu Cys Gln Ser Ala Gly Pro Phe Glu Ile Asn Met Glu Glu Thr

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360

365

atc tat cag aac tac caa cgt atc cgc atc cag gag agt ccc ggc aag 1152

Ile Tyr Gln Asn Tyr Gln Arg Ile Arg Ile Gln Glu Ser Pro Gly Lys

370

375

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gtg gcg gct ggc cga ctg ccc cgt tcc aag gat gcc att ctc ctc gct 1200

Val Ala Ala Gly Arg Leu Pro Arg Ser Lys Asp Ala Ile Leu Leu Ala

385

390

395

400

gat ctg gtg gac agc tgc aag cca ggg gac gag att gag ctg acc ggc 1248

Asp Leu Val Asp Ser Cys Lys Pro Gly Asp Glu Ile Glu Leu Thr Gly

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att tac cat aat aac tat gac ggc tcg ctt aac acc gcc aac ggc ttt 1296

Ile Tyr His Asn Asn Tyr Asp Gly Ser Leu Asn Thr Ala Asn Gly Phe

420

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cca gtc ttt gcc act att atc ttg gcc aac cat gtt gcc aag aag gac 1344

Pro Val Phe Ala Thr Ile Ile Leu Ala Asn His Val Ala Lys Lys Asp

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aac aaa gta gct gtg ggg gag ctc acc gat gag gac gtg aag atg atc 1392

Asn Lys Val Ala Val Gly Glu Leu Thr Asp Glu Asp Val Lys Met Ile

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455

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acc ggt ctc tcc aag gat cag caa att gga gag aag atc ttt gcc agc 1440

Thr Gly Leu Ser Lys Asp Gln Gln Ile Gly Glu Lys Ile Phe Ala Ser

465

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475

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att gca ccc tcc atc tat ggg cat gaa gac atc aag aga ggc ctg gct 1488

Ile Ala Pro Ser Ile Tyr Gly His Glu Asp Ile Lys Arg Gly Leu Ala

485

490

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ctg gcc ctg ttt gga ggg gag ccc aag aac cca ggt gga aag cac aag 1536

Leu Ala Leu Phe Gly Gly Glu Pro Lys Asn Pro Gly Gly Lys His Lys

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505

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gtt cga ggt gac att aat gtg ctc ttg tgt ggg gac cct ggc aca gca 1584

Val Arg Gly Asp Ile Asn Val Leu Leu Cys Gly Asp Pro Gly Thr Ala

515

520

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aag tcc caa ttc ctc aaa tac atc gag aaa gtg tct agc cgt gcc atc 1632

Lys Ser Gln Phe Leu Lys Tyr Ile Glu Lys Val Ser Ser Arg Ala Ile

530

535

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ttc acc act ggc cag ggt gcg tca gca gtg ggt ctc acc gcg tac gtt 1680

Phe Thr Thr Gly Gln Gly Ala Ser Ala Val Gly Leu Thr Ala Tyr Val

545

550

555

560

cag cgg cat ccc gtc agc aga gag tgg acc tta gag gcg gga gcc ctg 1728

Gln Arg His Pro Val Ser Arg Glu Trp Thr Leu Glu Ala Gly Ala Leu

565

570

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gtt ctg gct gac cgg ggg gtg tgt ctc att gac gag ttt gac aag atg 1776

Val Leu Ala Asp Arg Gly Val Cys Leu Ile Asp Glu Phe Asp Lys Met

580

585

590

aat gac cag gac agg acc agc atc cac gag gcc atg gaa cag caa agc 1824

Asn Asp Gln Asp Arg Thr Ser Ile His Glu Ala Met Glu Gln Gln Ser

595

600

605

atc tcc atc tcc aag gct ggc atc gtt acc tcg ctg caa gcc cgc tgc 1872

Ile Ser Ile Ser Lys Ala Gly Ile Val Thr Ser Leu Gln Ala Arg Cys

610

615

620

act gtc ata gct gct gcc aac ccc ata gga ggc cgc tac gac cct tca 1920

Thr Val Ile Ala Ala Ala Asn Pro Ile Gly Gly Arg Tyr Asp Pro Ser

625

630

635

640

ctg acc ttc tca gag aat gta gac ctc aca gag ccc atc att tcc cgc 1968

Leu Thr Phe Ser Glu Asn Val Asp Leu Thr Glu Pro Ile Ile Ser Arg

645

650

655

ttt gat gtc ctg tgt gtg gtg agg gac act gtt gat cca gtt cag gat 2016

Phe Asp Val Leu Cys Val Val Arg Asp Thr Val Asp Pro Val Gln Asp

660

665

670

gag atg ctg gcc cgc ttt gtg gtt ggc agc cac gtc aga cac cac ccc 2064

Glu Met Leu Ala Arg Phe Val Val Gly Ser His Val Arg His His Pro

675

680

685

agt aac aag aag gat gaa ggg ttg act aat ggt ggc acc ttg gag cca 2112

Ser Asn Lys Lys Asp Glu Gly Leu Thr Asn Gly Gly Thr Leu Glu Pro

690

695

700

gcc atg ccc aac aca tat ggc gtg gag ccc ctg cct cag gag gtg ctg 2160

Ala Met Pro Asn Thr Tyr Gly Val Glu Pro Leu Pro Gln Glu Val Leu

705

710

715

720

aag aag tat atc atc tat gcc aag gag agg gtc cgc ccg aag ctc aac 2208

Lys Lys Tyr Ile Ile Tyr Ala Lys Glu Arg Val Arg Pro Lys Leu Asn

725

730

735

cag atg gac cag gat aaa gtg gcc agg atg tac agt gac ctg agg aag 2256

Gln Met Asp Gln Asp Lys Val Ala Arg Met Tyr Ser Asp Leu Arg Lys

740

745

750

gag tcc atg gca acg ggc agc att ccc atc acg gtg cgc cac atc gag 2304

Glu Ser Met Ala Thr Gly Ser Ile Pro Ile Thr Val Arg His Ile Glu

755

760

765

tcc atg atc cgc atg gcc gag gcc cat gcc cgc atg cac ctg cgg gac 2352

Ser Met Ile Arg Met Ala Glu Ala His Ala Arg Met His Leu Arg Asp

770

775

780

tac gtg atg gaa gac gat gtc aac atg gcc atc cga gtg atg atg gag 2400

Tyr Val Met Glu Asp Asp Val Asn Met Ala Ile Arg Val Met Met Glu

785

790

795

800

agc ttc att gac acc cag aag ttc agc gtc atg cgg agt atg cgc aag 2448

Ser Phe Ile Asp Thr Gln Lys Phe Ser Val Met Arg Ser Met Arg Lys

805

810

815

act ttt gcc cgg tat ctc tcc ttc cgg cga gat aac aat gat ctg ctg 2496

Thr Phe Ala Arg Tyr Leu Ser Phe Arg Arg Asp Asn Asn Asp Leu Leu

820

825

830

ctc ttc ata ctg aag cag ttg gtg gct gag cag gtg aca tat caa cgc 2544

Leu Phe Ile Leu Lys Gln Leu Val Ala Glu Gln Val Thr Tyr Gln Arg

835

840

845

aac cgc ttt ggg gcc cag cag gac acc att gaa ata cct gag aag gat 2592

26 / 59

Asn Arg Phe Gly Ala Gln Gln Asp Thr Ile Glu Ile Pro Glu Lys Asp

850

855

860

ctg atg gac aag gcc agg cag atc aat att cac aac ctc tct gcc ttc 2640

Leu Met Asp Lys Ala Arg Gln Ile Asn Ile His Asn Leu Ser Ala Phe

865

870

875

880

tac gac agc gac ctc ttc aaa ttc aac aag ttc agc cgt gac ctg aaa 2688

Tyr Asp Ser Asp Leu Phe Lys Phe Asn Lys Phe Ser Arg Asp Leu Lys

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890

895

cgc aaa ctg atc cta cag cag ttc tga

2715

Arg Lys Leu Ile Leu Gln Gln Phe

900

905

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<213> Mus musculus

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Met Ala Glu Ser Ser Glu Ser Leu Ser Ala Ser Ser Pro Ala Arg Gln

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Arg Arg Arg Ile Ser Asp Pro Leu Thr Ser Ser Pro Gly Arg Ser Ser

20

25

30

27 / 59

Arg Arg Ala Asp Ala Leu Thr Ser Ser Pro Gly Arg Asp Leu Pro Pro

35

40

45

Phe Glu Asp Glu Ser Glu Gly Leu Leu Gly Thr Glu Gly Pro Met Glu

50

55

60

Glu Glu Glu Asp Gly Glu Glu Leu Ile Gly Asp Gly Met Glu Arg Asp

65

70

75

80

Tyr Arg Pro Ile Pro Glu Leu Asp Val Tyr Glu Ala Glu Gly Leu Ala

85

90

95

Leu Asp Asp Glu Asp Val Glu Glu Leu Thr Ala Ser Gln Arg Glu Ala

100

105

110

Ala Glu Arg Thr Met Arg Gln Arg Asp Arg Glu Ala Gly Arg Gly Leu

115

120

125

Gly Arg Met Arg Arg Gly Leu Leu Tyr Asp Ser Ser Glu Glu Asp Glu

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135

140

Glu Arg Pro Ala Arg Lys Arg Arg His Val Glu Arg Ala Thr Glu Asp

145

150

155

160

Gly Glu Glu Asp Glu Glu Met Ile Glu Ser Ile Glu Asn Leu Glu Asp

165

170

175

Leu Lys Gly His Ser Val Arg Glu Arg Val Ser Met Ala Gly Pro Arg

180

185

190

Leu Glu Ile His His Arg Phe Lys Asn Phe Leu Arg Thr His Val Asp

195

200

205

Ser His Gly His Asn Val Phe Lys Glu Arg Ile Ser Asp Met Cys Lys

210

215

220

Glu Asn Arg Glu Ser Leu Val Val Asn Tyr Glu Asp Leu Ala Ala Arg

225

230

235

240

Glu His Val Leu Ala Tyr Phe Leu Pro Glu Ala Pro Ala Glu Leu Leu

245

250

255

Gln Ile Phe Asp Glu Ala Ala Leu Glu Val Val Leu Ala Met Tyr Pro

260

265

270

Lys Tyr Asp Arg Ile Thr Asn His Ile His Val Arg Ile Ser His Leu

275

280

285

Pro Leu Val Glu Glu Leu Arg Ser Leu Arg Gln Leu His Leu Asn Gln

290

295

300

Leu Ile Arg Thr Ser Gly Val Val Thr Ser Cys Thr Gly Val Leu Pro

305

310

315

320

Gln Leu Ser Met Val Lys Tyr Asn Cys Ser Lys Cys Asn Phe Val Leu

325

330

335

Gly Pro Phe Cys Gln Ser Gln Asn Gln Glu Val Lys Pro Gly Ser Cys

340

345

350

Pro Glu Cys Gln Ser Ala Gly Pro Phe Glu Ile Asn Met Glu Glu Thr

355

360

365

Ile Tyr Gln Asn Tyr Gln Arg Ile Arg Ile Gln Glu Ser Pro Gly Lys

370

375

380

Val Ala Ala Gly Arg Leu Pro Arg Ser Lys Asp Ala Ile Leu Leu Ala

385

390

395

400

Asp Leu Val Asp Ser Cys Lys Pro Gly Asp Glu Ile Glu Leu Thr Gly

405

410

415

Ile Tyr His Asn Asn Tyr Asp Gly Ser Leu Asn Thr Ala Asn Gly Phe

420

425

430

Pro Val Phe Ala Thr Ile Ile Leu Ala Asn His Val Ala Lys Lys Asp

435

440

445

Asn Lys Val Ala Val Gly Glu Leu Thr Asp Glu Asp Val Lys Met Ile

450

455

460

Thr Gly Leu Ser Lys Asp Gln Gln Ile Gly Glu Lys Ile Phe Ala Ser

465

470

475

480

Ile Ala Pro Ser Ile Tyr Gly His Glu Asp Ile Lys Arg Gly Leu Ala

485

490

495

Leu Ala Leu Phe Gly Gly Glu Pro Lys Asn Pro Gly Gly Lys His Lys

500

505

510

Val Arg Gly Asp Ile Asn Val Leu Leu Cys Gly Asp Pro Gly Thr Ala

515

520

525

Lys Ser Gln Phe Leu Lys Tyr Ile Glu Lys Val Ser Ser Arg Ala Ile

530

535

540

Phe Thr Thr Gly Gln Gly Ala Ser Ala Val Gly Leu Thr Ala Tyr Val

545

550

555

560

Gln Arg His Pro Val Ser Arg Glu Trp Thr Leu Glu Ala Gly Ala Leu

565

570

575

Val Leu Ala Asp Arg Gly Val Cys Leu Ile Asp Glu Phe Asp Lys Met

580

585

590

Asn Asp Gln Asp Arg Thr Ser Ile His Glu Ala Met Glu Gln Gln Ser

595

600

605

Ile Ser Ile Ser Lys Ala Gly Ile Val Thr Ser Leu Gln Ala Arg Cys

610

615

620

Thr Val Ile Ala Ala Ala Asn Pro Ile Gly Gly Arg Tyr Asp Pro Ser

625

630

635

640

Leu Thr Phe Ser Glu Asn Val Asp Leu Thr Glu Pro Ile Ile Ser Arg

645

650

655

Phe Asp Val Leu Cys Val Val Arg Asp Thr Val Asp Pro Val Gln Asp

660

665

670

Glu Met Leu Ala Arg Phe Val Val Gly Ser His Val Arg His His Pro

675

680

685

Ser Asn Lys Lys Asp Glu Gly Leu Thr Asn Gly Gly Thr Leu Glu Pro

690

695

700

Ala Met Pro Asn Thr Tyr Gly Val Glu Pro Leu Pro Gln Glu Val Leu

705

710

715

720

Lys Lys Tyr Ile Ile Tyr Ala Lys Glu Arg Val Arg Pro Lys Leu Asn

725

730

735

Gln Met Asp Gln Asp Lys Val Ala Arg Met Tyr Ser Asp Leu Arg Lys

740

745

750

Glu Ser Met Ala Thr Gly Ser Ile Pro Ile Thr Val Arg His Ile Glu

755

760

765

Ser Met Ile Arg Met Ala Glu Ala His Ala Arg Met His Leu Arg Asp

770

775

780

Tyr Val Met Glu Asp Asp Val Asn Met Ala Ile Arg Val Met Met Glu

785

790

795

800

Ser Phe Ile Asp Thr Gln Lys Phe Ser Val Met Arg Ser Met Arg Lys

805

810

815

Thr Phe Ala Arg Tyr Leu Ser Phe Arg Arg Asp Asn Asn Asp Leu Leu

820

825

830

Leu Phe Ile Leu Lys Gln Leu Val Ala Glu Gln Val Thr Tyr Gln Arg

835

840

845

Asn Arg Phe Gly Ala Gln Gln Asp Thr Ile Glu Ile Pro Glu Lys Asp

850

855

860

31 / 59

Leu Met Asp Lys Ala Arg Gln Ile Asn Ile His Asn Leu Ser Ala Phe

865

870

875

880

Tyr Asp Ser Asp Leu Phe Lys Phe Asn Lys Phe Ser Arg Asp Leu Lys

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890

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Arg Lys Leu Ile Leu Gln Gln Phe

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aattggcttg tg atg gag gcg tct ttg ggg att cag atg gat gag cca atg 171

Met Glu Ala Ser Leu Gly Ile Gln Met Asp Glu Pro Met

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5

10

gct ttt tct ccc cag cgt gac cgg ttt cag gct gaa ggc tct tta aaa 219

3 2 / 5 9

Ala Phe Ser Pro Gln Arg Asp Arg Phe Gln Ala Glu Gly Ser Leu Lys

15

20

25

aaa aac gag cag aat ttt aaa ctt gca ggt gtt aaa aaa gat att gag 267

Lys Asn Glu Gln Asn Phe Lys Leu Ala Gly Val Lys Lys Asp Ile Glu

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aag ctt tat gaa gct gta cca cag ctt agt aat gtg ttt aag att gag 315

Lys Leu Tyr Glu Ala Val Pro Gln Leu Ser Asn Val Phe Lys Ile Glu

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gac aaa att gga gaa ggc act ttc agc tct gtt tat ttg gcc aca gca 363

Asp Lys Ile Gly Glu Gly Thr Phe Ser Ser Val Tyr Leu Ala Thr Ala

65

70

75

cag tta caa gta gga cct gaa gag aaa att gct cta aaa cac ttg att 411

Gln Leu Gln Val Gly Pro Glu Glu Lys Ile Ala Leu Lys His Leu Ile

80

85

90

cca aca agt cat cct ata aga att gca gct gaa ctt cag tgc cta aca 459

Pro Thr Ser His Pro Ile Arg Ile Ala Ala Glu Leu Gln Cys Leu Thr

95

100

105

gtg gct ggg ggg caa gat aat gtc atg gga gtt aaa tac tgc ttt agg 507

Val Ala Gly Gly Gln Asp Asn Val Met Gly Val Lys Tyr Cys Phe Arg

110

115

120

125

aag aat gat cat gta gtt att gct atg cca tat ctg gag cat gag tcg 555

Lys Asn Asp His Val Val Ile Ala Met Pro Tyr Leu Glu His Glu Ser

130

135

140

ttt ttg gac att ctg aat tct ctt tcc ttt caa gaa gta cgg gaa tat 603

Phe Leu Asp Ile Leu Asn Ser Leu Ser Phe Gln Glu Val Arg Glu Tyr

145

150

155

atg ctt aat ctg ttc aaa gct ttg aaa cgc att cat cag ttt ggt att 651

Met Leu Asn Leu Phe Lys Ala Leu Lys Arg Ile His Gln Phe Gly Ile

160

165

170

gtt cac cgt gat gtt aag ccc agc aat ttt tta tat aat agg cgc ctg 699

Val His Arg Asp Val Lys Pro Ser Asn Phe Leu Tyr Asn Arg Arg Leu

175

180

185

aaa aag tat gcc ttg gta gac ttt ggt ttg gcc caa gga acc cat gat 747

Lys Lys Tyr Ala Leu Val Asp Phe Gly Leu Ala Gln Gly Thr His Asp

190

195

200

205

acg aaa ata gag ctt ctt aaa ttt gtc cag tct gaa gct cag cag gaa 795

Thr Lys Ile Glu Leu Leu Lys Phe Val Gln Ser Glu Ala Gln Gln Glu

210

215

220

agg tgt tca caa aac aaa tcc cac ata atc aca gga aac aag att cca 843

Arg Cys Ser Gln Asn Lys Ser His Ile Ile Thr Gly Asn Lys Ile Pro

225

230

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ctg agt ggc cca gta cct aag gag ctg gat cag cag tcc acc aca aaa 891

Leu Ser Gly Pro Val Pro Lys Glu Leu Asp Gln Gln Ser Thr Thr Lys

240

245

250

gct tct gtt aaa aga ccc tac aca aat gca caa att cag att aaa caa 939

Ala Ser Val Lys Arg Pro Tyr Thr Asn Ala Gln Ile Gln Ile Lys Gln

255

260

265

gga aaa gac gga aag gag gga tct gta ggc ctt tct gtc cag cgc tct 987

Gly Lys Asp Gly Lys Glu Gly Ser Val Gly Leu Ser Val Gln Arg Ser

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275

280

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gtt ttt gga gaa aga aat ttc aat ata cac agc tcc att tca cat gag 1035

Val Phe Gly Glu Arg Asn Phe Asn Ile His Ser Ser Ile Ser His Glu

290

295

300

agc cct gca gtg aaa ctc atg aag cag tca aag act gtg gat gta ctg 1083

Ser Pro Ala Val Lys Leu Met Lys Gln Ser Lys Thr Val Asp Val Leu

305

310

315

tct aga aag tta gca aca aaa aag aag gct att tct acg aaa gtt atg 1131

Ser Arg Lys Leu Ala Thr Lys Lys Lys Ala Ile Ser Thr Lys Val Met

320

325

330

aat agt gct gtg atg agg aaa act gcc agt tct tgc cca gct agc ctg 1179

Asn Ser Ala Val Met Arg Lys Thr Ala Ser Ser Cys Pro Ala Ser Leu

335

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acc tgt gac tgc tat gca aca gat aaa gtt tgt agt att tgc ctt tca 1227

Thr Cys Asp Cys Tyr Ala Thr Asp Lys Val Cys Ser Ile Cys Leu Ser

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355

360

365

agg cgt cag cag gtt gcc cct agg gca ggt aca cca gga ttc aga gca 1275

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370

375

380

cca gag gtc ttg aca aag tgc ccc aat caa act aca gca att gac atg 1323

Pro Glu Val Leu Thr Lys Cys Pro Asn Gln Thr Thr Ala Ile Asp Met

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390

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tgg tct gca ggt gtc ata ttt ctt tct ttg ctt agt gga cga tat cca 1371

Trp Ser Ala Gly Val Ile Phe Leu Ser Leu Leu Ser Gly Arg Tyr Pro

400

405

410

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Phe Tyr Lys Ala Ser Asp Asp Leu Thr Ala Leu Ala Gln Ile Met Thr

415

420

425

att agg gga tcc aga gaa act atc caa gct gct aaa act ttt ggg aaa 1467

Ile Arg Gly Ser Arg Glu Thr Ile Gln Ala Ala Lys Thr Phe Gly Lys

430

435

440

445

tca ata tta tgt agc aaa gaa gtt cca gca caa gac ttg aga aaa ctc 1515

Ser Ile Leu Cys Ser Lys Glu Val Pro Ala Gln Asp Leu Arg Lys Leu

450

455

460

tgt gag aga ctc agg ggt atg gat tct agc act ccc aag tta aca agt 1563

Cys Glu Arg Leu Arg Gly Met Asp Ser Ser Thr Pro Lys Leu Thr Ser

465

470

475

gat ata caa ggg cat gct tct cat caa cca gct att tca gag aag act 1611

Asp Ile Gln Gly His Ala Ser His Gln Pro Ala Ile Ser Glu Lys Thr

480

485

490

gac cat aaa gct tct tgc ctc gtt caa aca cct cca gga caa tac tca 1659

Asp His Lys Ala Ser Cys Leu Val Gln Thr Pro Pro Gly Gln Tyr Ser

495

500

505

ggg aat tca ttt aaa aag ggg gat agt aat agc tgt gag cat tgt ttt 1707

Gly Asn Ser Phe Lys Lys Gly Asp Ser Asn Ser Cys Glu His Cys Phe

510

515

520

525

gat gag tat aat acc aat tta gaa ggc tgg aat gag gta cct gat gaa 1755

Asp Glu Tyr Asn Thr Asn Leu Glu Gly Trp Asn Glu Val Pro Asp Glu

530

535

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gct tat gac ctg ctt gat aaa ctt cta gat cta aat cca gct tca aga 1803  
 Ala Tyr Asp Leu Leu Asp Lys Leu Leu Asp Leu Asn Pro Ala Ser Arg  
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ata aca gca gaa gaa gct ttg ttg cat cca ttt ttt aaa gat atg agc 1851  
 Ile Thr Ala Glu Glu Ala Leu Leu His Pro Phe Phe Lys Asp Met Ser  
 560 565 570

ttg tga taatggatct tcatttaatg tttactgtta tgaggtagaa taaaaagaa 1907  
 Leu  
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<212> PRT

<213> Homo sapiens

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Pro Gln Arg Asp Arg Phe Gln Ala Glu Gly Ser Leu Lys Lys Asn Glu

20

25

30

Gln Asn Phe Lys Leu Ala Gly Val Lys Lys Asp Ile Glu Lys Leu Tyr

35

40

45

Glu Ala Val Pro Gln Leu Ser Asn Val Phe Lys Ile Glu Asp Lys Ile

50

55

60

Gly Glu Gly Thr Phe Ser Ser Val Tyr Leu Ala Thr Ala Gln Leu Gln

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65	70	75	80
Val Gly Pro Glu Glu Lys Ile Ala Leu Lys His Leu Ile Pro Thr Ser			
	85	90	95
His Pro Ile Arg Ile Ala Ala Glu Leu Gln Cys Leu Thr Val Ala Gly			
	100	105	110
Gly Gln Asp Asn Val Met Gly Val Lys Tyr Cys Phe Arg Lys Asn Asp			
	115	120	125
His Val Val Ile Ala Met Pro Tyr Leu Glu His Glu Ser Phe Leu Asp			
	130	135	140
Ile Leu Asn Ser Leu Ser Phe Gln Glu Val Arg Glu Tyr Met Leu Asn			
145	150	155	160
Leu Phe Lys Ala Leu Lys Arg Ile His Gln Phe Gly Ile Val His Arg			
	165	170	175
Asp Val Lys Pro Ser Asn Phe Leu Tyr Asn Arg Arg Leu Lys Lys Tyr			
	180	185	190
Ala Leu Val Asp Phe Gly Leu Ala Gln Gly Thr His Asp Thr Lys Ile			
	195	200	205
Glu Leu Leu Lys Phe Val Gln Ser Glu Ala Gln Gln Glu Arg Cys Ser			
	210	215	220
Gln Asn Lys Ser His Ile Ile Thr Gly Asn Lys Ile Pro Leu Ser Gly			
225	230	235	240
Pro Val Pro Lys Glu Leu Asp Gln Gln Ser Thr Thr Lys Ala Ser Val			
	245	250	255
Lys Arg Pro Tyr Thr Asn Ala Gln Ile Gln Ile Lys Gln Gly Lys Asp			
	260	265	270
Gly Lys Glu Gly Ser Val Gly Leu Ser Val Gln Arg Ser Val Phe Gly			

275	280	285	
Glu Arg Asn Phe Asn Ile His Ser Ser Ile Ser His Glu Ser Pro Ala			
290	295	300	
Val Lys Leu Met Lys Gln Ser Lys Thr Val Asp Val Leu Ser Arg Lys			
305	310	315	320
Leu Ala Thr Lys Lys Lys Ala Ile Ser Thr Lys Val Met Asn Ser Ala			
	325	330	335
Val Met Arg Lys Thr Ala Ser Ser Cys Pro Ala Ser Leu Thr Cys Asp			
	340	345	350
Cys Tyr Ala Thr Asp Lys Val Cys Ser Ile Cys Leu Ser Arg Arg Gln			
	355	360	365
Gln Val Ala Pro Arg Ala Gly Thr Pro Gly Phe Arg Ala Pro Glu Val			
	370	375	380
Leu Thr Lys Cys Pro Asn Gln Thr Thr Ala Ile Asp Met Trp Ser Ala			
385	390	395	400
Gly Val Ile Phe Leu Ser Leu Leu Ser Gly Arg Tyr Pro Phe Tyr Lys			
	405	410	415
Ala Ser Asp Asp Leu Thr Ala Leu Ala Gln Ile Met Thr Ile Arg Gly			
	420	425	430
Ser Arg Glu Thr Ile Gln Ala Ala Lys Thr Phe Gly Lys Ser Ile Leu			
	435	440	445
Cys Ser Lys Glu Val Pro Ala Gln Asp Leu Arg Lys Leu Cys Glu Arg			
	450	455	460
Leu Arg Gly Met Asp Ser Ser Thr Pro Lys Leu Thr Ser Asp Ile Gln			
465	470	475	480
Gly His Ala Ser His Gln Pro Ala Ile Ser Glu Lys Thr Asp His Lys			

41 / 59

485	490	495
Ala Ser Cys Leu Val Gln Thr Pro Pro Gly Gln Tyr Ser Gly Asn Ser		
500	505	510
Phe Lys Lys Gly Asp Ser Asn Ser Cys Glu His Cys Phe Asp Glu Tyr		
515	520	525
Asn Thr Asn Leu Glu Gly Trp Asn Glu Val Pro Asp Glu Ala Tyr Asp		
530	535	540
Leu Leu Asp Lys Leu Leu Asp Leu Asn Pro Ala Ser Arg Ile Thr Ala		
545	550	555
Glu Glu Ala Leu Leu His Pro Phe Phe Lys Asp Met Ser Leu		560
565	570	

<210> 8

<211> 2780

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (518).. (2542)

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gtctgagact gagagagcaa cggaatggag gcggggtaga ggcggaaaca caacctgcag 120  
ggccagagcg aggcgcgaga aggacggcgg cgtgaggggg cggggcgcgc agcgcgagaa 180

ggcaggcacg aggggcgagc gcgaggcggg gcacggcgcg tggcgtgaga cggggcgggg 240  
 cgcgcgtatc ggccgcgcgg ccgcgtgacg cgttttcaaa tcttcaaccg ccgcagccca 300  
 ctcgtttgtg ctttgcgcct tctcctcccg cgccttgag cggatccgg ccccgaaac 360  
 ccgacctgca gacgcggtac ctctactgcg tagaggccgt agctggcgga aggagagagg 420  
 cggccgtcct gtcaacaggc cgggggaagc cgtgctttcg cggctgcccg gtgcgacact 480

ttctccggac ccagcatgta ggtgccgggc gactgcc atg aac tcc gga gcc atg 535

Met Asn Ser Gly Ala Met

1

5

agg atc cac agt aaa gga cat ttc cag ggt gga atc caa gtc aaa aat 583

Arg Ile His Ser Lys Gly His Phe Gln Gly Gly Ile Gln Val Lys Asn

10

15

20

gaa aaa aac aga cca tct ctg aaa tct ctg aaa act gat aac agg cca 631

Glu Lys Asn Arg Pro Ser Leu Lys Ser Leu Lys Thr Asp Asn Arg Pro

25

30

35

gaa aaa tcc aaa tgt aag cca ctt tgg gga aaa gta ttt tac ctt gac 679

Glu Lys Ser Lys Cys Lys Pro Leu Trp Gly Lys Val Phe Tyr Leu Asp

40

45

50

tta cct tct gtc acc ata tct gaa aaa ctt caa aag gac att aag gat 727

Leu Pro Ser Val Thr Ile Ser Glu Lys Leu Gln Lys Asp Ile Lys Asp

55

60

65

70

ctg gga ggg cga gtt gaa gaa ttt ctc agc aaa gat atc agt tat ctt 775

Leu Gly Gly Arg Val Glu Glu Phe Leu Ser Lys Asp Ile Ser Tyr Leu

75

80

85

att tca aat aag aag gaa gct aaa ttt gca caa acc ttg ggt cga att 823

Ile Ser Asn Lys Lys Glu Ala Lys Phe Ala Gln Thr Leu Gly Arg Ile

90

95

100

tct cct gta cca agt cca gaa tct gca tat act gca gaa acc act tca 871

Ser Pro Val Pro Ser Pro Glu Ser Ala Tyr Thr Ala Glu Thr Thr Ser

105

110

115

cct cat ccc agc cat gat gga agt tca ttt aag tca cca gac aca gtg 919

Pro His Pro Ser His Asp Gly Ser Ser Phe Lys Ser Pro Asp Thr Val

120

125

130

tgt tta agc aga gga aaa tta tta gtt gaa aaa gct atc aag gac cat 967

Cys Leu Ser Arg Gly Lys Leu Leu Val Glu Lys Ala Ile Lys Asp His

135

140

145

150

gat ttt att cct tca aat agt ata tta tca aat gcc ttg tca tgg gga 1015

Asp Phe Ile Pro Ser Asn Ser Ile Leu Ser Asn Ala Leu Ser Trp Gly

155

160

165

gta aaa att ctt cat att gat gac att aga tac tac att gaa caa aag 1063

Val Lys Ile Leu His Ile Asp Asp Ile Arg Tyr Tyr Ile Glu Gln Lys

44 / 59

170

175

180

aaa aaa gag ttg tat tta ctc aag aaa tca agt act tca gta aga gat 1111

Lys Lys Glu Leu Tyr Leu Leu Lys Lys Ser Ser Thr Ser Val Arg Asp

185

190

195

ggg ggc aaa aga gtt ggt agt ggt gca caa aaa aca aga aca gga aga 1159

Gly Gly Lys Arg Val Gly Ser Gly Ala Gln Lys Thr Arg Thr Gly Arg

200

205

210

ctc aaa aag cct ttt gta aag gtg gaa gat atg agc caa ctt tat agg 1207

Leu Lys Lys Pro Phe Val Lys Val Glu Asp Met Ser Gln Leu Tyr Arg

215

220

225

230

cca ttt tat ctt cag ctg acc aat atg cct ttt ata aat tat tct att 1255

Pro Phe Tyr Leu Gln Leu Thr Asn Met Pro Phe Ile Asn Tyr Ser Ile

235

240

245

cag aag ccc tgc agt cca ttt gat gta gac aag cca tct agt atg caa 1303

Gln Lys Pro Cys Ser Pro Phe Asp Val Asp Lys Pro Ser Ser Met Gln

250

255

260

aag caa act cag gtt aaa cta aga atc caa aca gat ggc gat aag tat 1351

Lys Gln Thr Gln Val Lys Leu Arg Ile Gln Thr Asp Gly Asp Lys Tyr

265

270

275

ggt gga acc tca att caa ctc cag ttg aaa gag aag aag aaa aaa gga 1399

Gly Gly Thr Ser Ile Gln Leu Gln Leu Lys Glu Lys Lys Lys Lys Gly

280

285

290

tat tgt gaa tgt tgc ttg cag aaa tat gaa gat cta gaa act cac ctt 1447

Tyr Cys Glu Cys Cys Leu Gln Lys Tyr Glu Asp Leu Glu Thr His Leu

295

300

305

310

cta agt gag caa cac aga aac ttt gca cag agt aac cag tat caa gtt 1495

Leu Ser Glu Gln His Arg Asn Phe Ala Gln Ser Asn Gln Tyr Gln Val

315

320

325

gtt gat gat att gta tct aag tta gtt ttt gac ttt gtg gaa tat gaa 1543

Val Asp Asp Ile Val Ser Lys Leu Val Phe Asp Phe Val Glu Tyr Glu

330

335

340

aag gac aca cct aaa aag aaa aga ata aaa tac agt gtt gga tcc ctt 1591

Lys Asp Thr Pro Lys Lys Lys Arg Ile Lys Tyr Ser Val Gly Ser Leu

345

350

355

tct cct gtt tct gca agt gtc ctg aaa aag act gaa caa aag gaa aaa 1639

Ser Pro Val Ser Ala Ser Val Leu Lys Lys Thr Glu Gln Lys Glu Lys

360

365

370

gtg gaa ttg caa cat att tct cag aaa gat tgc cag gaa gat gat aca 1687

Val Glu Leu Gln His Ile Ser Gln Lys Asp Cys Gln Glu Asp Asp Thr

375

380

385

390

aca gtg aag gag cag aat ttc ctg tat aaa gag acc cag gaa act gaa 1735

Thr Val Lys Glu Gln Asn Phe Leu Tyr Lys Glu Thr Gln Glu Thr Glu

395

400

405

aaa aag ctc ctg ttt att tca gag ccc atc ccc cac cct tca aat gaa 1783

Lys Lys Leu Leu Phe Ile Ser Glu Pro Ile Pro His Pro Ser Asn Glu

410

415

420

ttg aga ggg ctt aat gag aaa atg agt aat aaa tgt tcc atg tta agt 1831

Leu Arg Gly Leu Asn Glu Lys Met Ser Asn Lys Cys Ser Met Leu Ser

425

430

435

aca gct gaa gat gac ata aga cag aat ttt aca cag cta cct cta cat 1879

Thr Ala Glu Asp Asp Ile Arg Gln Asn Phe Thr Gln Leu Pro Leu His

440

445

450

aaa aac aaa cag gaa tgc att ctt gac att tcc gaa cac aca tta agt 1927

Lys Asn Lys Gln Glu Cys Ile Leu Asp Ile Ser Glu His Thr Leu Ser

455

460

465

470

gaa aat gac tta gaa gaa cta agg gta gat cac tat aaa tgt aac ata 1975

Glu Asn Asp Leu Glu Glu Leu Arg Val Asp His Tyr Lys Cys Asn Ile

475

480

485

cag gca tct gta cat gtt tct gat ttc agt aca gat aat agt gga tct 2023

Gln Ala Ser Val His Val Ser Asp Phe Ser Thr Asp Asn Ser Gly Ser

490

495

500

caa cca aaa cag aag tca gat act gtg ctt ttt cca gca aag gat ctc 2071

Gln Pro Lys Gln Lys Ser Asp Thr Val Leu Phe Pro Ala Lys Asp Leu

505

510

515

aag gaa aag gac ctt cat tca ata ttt act cat gat tct ggt ctg ata 2119

Lys Glu Lys Asp Leu His Ser Ile Phe Thr His Asp Ser Gly Leu Ile

520

525

530

aca ata aac agt tca caa gag cac cta act gtt cag gca aag gct cca 2167

Thr Ile Asn Ser Ser Gln Glu His Leu Thr Val Gln Ala Lys Ala Pro

535

540

545

550

ttc cat act cct cct gag gaa ccc aat gaa tgt gac ttc aag aat atg 2215

Phe His Thr Pro Pro Glu Glu Pro Asn Glu Cys Asp Phe Lys Asn Met

555

560

565

gat agt tta cct tct ggt aaa ata cat cga aaa gtg aaa ata ata tta 2263

Asp Ser Leu Pro Ser Gly Lys Ile His Arg Lys Val Lys Ile Ile Leu

570

575

580

gga cga aat aga aaa gaa aat ctg gaa cca aat gct gaa ttt gat aaa 2311

Gly Arg Asn Arg Lys Glu Asn Leu Glu Pro Asn Ala Glu Phe Asp Lys

585

590

595

aga act gaa ttt att aca caa gaa gaa aac aga att tgt agt tca ccg 2359

Arg Thr Glu Phe Ile Thr Gln Glu Glu Asn Arg Ile Cys Ser Ser Pro

600

605

610

gta cag tct tta cta gac ttg ttt cag act agt gaa gag aaa tca gaa 2407

Val Gln Ser Leu Leu Asp Leu Phe Gln Thr Ser Glu Glu Lys Ser Glu

615

620

625

630

ttt ttg ggt ttc aca agc tac aca gaa aag agt ggt ata tgc aat gtt 2455

Phe Leu Gly Phe Thr Ser Tyr Thr Glu Lys Ser Gly Ile Cys Asn Val

635

640

645

tta gat att tgg gaa gag gaa aat tca gat aat ctg tta aca gcg ttt 2503

Leu Asp Ile Trp Glu Glu Glu Asn Ser Asp Asn Leu Leu Thr Ala Phe

650

655

660

ttc tcg tcc cct tca act tct aca ttt act ggc ttt tag aatttaaaaa 2552

Phe Ser Ser Pro Ser Thr Ser Thr Phe Thr Gly Phe

665

670

675

atgcatactt ttcagaagtg ataaggatca tattcttgaa atttttataa atatgtatgg 2612

aaattcttag gattttttta ccagctttgt ttacagaccc aaatgtaaata attaaaaata 2672

aatatttgca attttctaca gaattgaata cctgttaaag aaaaattaca gaataaactt 2732

gtgactggtc ttgttttaca ttataaaaaa aaaaaaaaaa aactcgag 2780

&lt;210&gt; 9

&lt;211&gt; 674

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 9

Met Asn Ser Gly Ala Met Arg Ile His Ser Lys Gly His Phe Gln Gly

1 5 10 15

Gly Ile Gln Val Lys Asn Glu Lys Asn Arg Pro Ser Leu Lys Ser Leu

20 25 30

Lys Thr Asp Asn Arg Pro Glu Lys Ser Lys Cys Lys Pro Leu Trp Gly

35 40 45

Lys Val Phe Tyr Leu Asp Leu Pro Ser Val Thr Ile Ser Glu Lys Leu

50 55 60

Gln Lys Asp Ile Lys Asp Leu Gly Gly Arg Val Glu Glu Phe Leu Ser

65 70 75 80

Lys Asp Ile Ser Tyr Leu Ile Ser Asn Lys Lys Glu Ala Lys Phe Ala

85 90 95

Gln Thr Leu Gly Arg Ile Ser Pro Val Pro Ser Pro Glu Ser Ala Tyr

100 105 110

Thr Ala Glu Thr Thr Ser Pro His Pro Ser His Asp Gly Ser Ser Phe

115 120 125

Lys Ser Pro Asp Thr Val Cys Leu Ser Arg Gly Lys Leu Leu Val Glu

130 135 140

Lys Ala Ile Lys Asp His Asp Phe Ile Pro Ser Asn Ser Ile Leu Ser  
 145                      150                      155                      160  
 Asn Ala Leu Ser Trp Gly Val Lys Ile Leu His Ile Asp Asp Ile Arg  
                          165                      170                      175  
 Tyr Tyr Ile Glu Gln Lys Lys Lys Glu Leu Tyr Leu Leu Lys Lys Ser  
                          180                      185                      190  
 Ser Thr Ser Val Arg Asp Gly Gly Lys Arg Val Gly Ser Gly Ala Gln  
                          195                      200                      205  
 Lys Thr Arg Thr Gly Arg Leu Lys Lys Pro Phe Val Lys Val Glu Asp  
                          210                      215                      220  
 Met Ser Gln Leu Tyr Arg Pro Phe Tyr Leu Gln Leu Thr Asn Met Pro  
 225                      230                      235                      240  
 Phe Ile Asn Tyr Ser Ile Gln Lys Pro Cys Ser Pro Phe Asp Val Asp  
                          245                      250                      255  
 Lys Pro Ser Ser Met Gln Lys Gln Thr Gln Val Lys Leu Arg Ile Gln  
                          260                      265                      270  
 Thr Asp Gly Asp Lys Tyr Gly Gly Thr Ser Ile Gln Leu Gln Leu Lys  
                          275                      280                      285  
 Glu Lys Lys Lys Lys Gly Tyr Cys Glu Cys Cys Leu Gln Lys Tyr Glu  
                          290                      295                      300  
 Asp Leu Glu Thr His Leu Leu Ser Glu Gln His Arg Asn Phe Ala Gln  
 305                      310                      315                      320  
 Ser Asn Gln Tyr Gln Val Val Asp Asp Ile Val Ser Lys Leu Val Phe  
                          325                      330                      335  
 Asp Phe Val Glu Tyr Glu Lys Asp Thr Pro Lys Lys Lys Arg Ile Lys  
                          340                      345                      350

Tyr Ser Val Gly Ser Leu Ser Pro Val Ser Ala Ser Val Leu Lys Lys

355

360

365

Thr Glu Gln Lys Glu Lys Val Glu Leu Gln His Ile Ser Gln Lys Asp

370

375

380

Cys Gln Glu Asp Asp Thr Thr Val Lys Glu Gln Asn Phe Leu Tyr Lys

385

390

395

400

Glu Thr Gln Glu Thr Glu Lys Lys Leu Leu Phe Ile Ser Glu Pro Ile

405

410

415

Pro His Pro Ser Asn Glu Leu Arg Gly Leu Asn Glu Lys Met Ser Asn

420

425

430

Lys Cys Ser Met Leu Ser Thr Ala Glu Asp Asp Ile Arg Gln Asn Phe

435

440

445

Thr Gln Leu Pro Leu His Lys Asn Lys Gln Glu Cys Ile Leu Asp Ile

450

455

460

Ser Glu His Thr Leu Ser Glu Asn Asp Leu Glu Glu Leu Arg Val Asp

465

470

475

480

His Tyr Lys Cys Asn Ile Gln Ala Ser Val His Val Ser Asp Phe Ser

485

490

495

Thr Asp Asn Ser Gly Ser Gln Pro Lys Gln Lys Ser Asp Thr Val Leu

500

505

510

Phe Pro Ala Lys Asp Leu Lys Glu Lys Asp Leu His Ser Ile Phe Thr

515

520

525

His Asp Ser Gly Leu Ile Thr Ile Asn Ser Ser Gln Glu His Leu Thr

530

535

540

Val Gln Ala Lys Ala Pro Phe His Thr Pro Pro Glu Glu Pro Asn Glu

545

550

555

560

5 2 / 5 9

Cys Asp Phe Lys Asn Met Asp Ser Leu Pro Ser Gly Lys Ile His Arg

565

570

575

Lys Val Lys Ile Ile Leu Gly Arg Asn Arg Lys Glu Asn Leu Glu Pro

580

585

590

Asn Ala Glu Phe Asp Lys Arg Thr Glu Phe Ile Thr Gln Glu Glu Asn

595

600

605

Arg Ile Cys Ser Ser Pro Val Gln Ser Leu Leu Asp Leu Phe Gln Thr

610

615

620

Ser Glu Glu Lys Ser Glu Phe Leu Gly Phe Thr Ser Tyr Thr Glu Lys

625

630

635

640

Ser Gly Ile Cys Asn Val Leu Asp Ile Trp Glu Glu Glu Asn Ser Asp

645

650

655

Asn Leu Leu Thr Ala Phe Phe Ser Ser Pro Ser Thr Ser Thr Phe Thr

660

665

670

Gly Phe

<210> 10

<211> 176

<212> PRT

<213> Homo sapiens

<400> 10

Asp Ile Arg Tyr Tyr Ile Glu Gln Lys Lys Lys Glu Leu Tyr Leu Leu

1

5

10

15

53 / 59

Lys Lys Ser Ser Thr Ser Val Arg Asp Gly Gly Lys Arg Val Gly Ser

20

25

30

Gly Ala Gln Lys Thr Arg Thr Gly Arg Leu Lys Lys Pro Phe Val Lys

35

40

45

Val Glu Asp Met Ser Gln Leu Tyr Arg Pro Phe Tyr Leu Gln Leu Thr

50

55

60

Asn Met Pro Phe Ile Asn Tyr Ser Ile Gln Lys Pro Cys Ser Pro Phe

65

70

75

80

Asp Val Asp Lys Pro Ser Ser Met Gln Lys Gln Thr Gln Val Lys Leu

85

90

95

Arg Ile Gln Thr Asp Gly Asp Lys Tyr Gly Gly Thr Ser Ile Gln Leu

100

105

110

Gln Leu Lys Glu Lys Lys Lys Lys Gly Tyr Cys Glu Cys Cys Leu Gln

115

120

125

Lys Tyr Glu Asp Leu Glu Thr His Leu Leu Ser Glu Gln His Arg Asn

130

135

140

Phe Ala Gln Ser Asn Gln Tyr Gln Val Val Asp Asp Ile Val Ser Lys

5 4 / 5 9

145

150

155

160

Leu Val Phe Asp Phe Val Glu Tyr Glu Lys Asp Thr Pro Lys Lys Lys

165

170

175

<210> 11

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially  
synthesized primer sequence

<400> 11

cccaagcttg acattagata ctacattgaa

30

<210> 12

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially

synthesized primer sequence

<400> 12

ccggaattct ttcttttttag gtgtgtcctt

30

<210> 13

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:TAT sequence

<400> 13

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg

1

5

10

<210> 14

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially

synthesized adaptor sequence

<400> 14

aattgcggcc gc

12

<210> 15

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially  
synthesized primer sequence

<400> 15

ataagaatgc ggccgctaag aaggagatat acatatgtac ccctacgacg tg

52

<210> 16

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially

5 7 / 5 9

synthesized primer sequence

<400> 16

ataagaatgc ggccgcttat cacaagctca tatcttt

37

<210> 17

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially  
synthesized peptide sequence

<400> 17

Met Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Phe Ser Pro Gln Arg Asp

1

5

10

15

<210> 18

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially  
synthesized primer sequence

<400> 18

cacggatcca tggcatccag cccggccca

29

<210> 19

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially  
synthesized primer sequence

<400> 19

gtgctcgagc atcgctgtca tacaggagcc

30

<210> 20

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially  
synthesized peptide sequence

<220>

<221> MOD\_RES

<222> (9)

<223> PHOSPHORYLATION

<400> 20

Cys Arg Gly Asn Asp Pro Leu Thr Ser Ser

1 5 10

<210> 21

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially  
synthesized peptide sequence

<400> 21

Cys Arg Gly Asn Asp Pro Leu Thr Ser Ser

1 5 10